87940

**STIC-Biotech/ChemLib**

**From:** Schultz, James
**Sent:** Monday, March 03, 2003 11:07 AM
**T :** STIC-Biotech/ChemLib
**Subject:** sequence search request for 10/003,919

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO:3 (5273 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 50 nucleotides.
Thank you very much,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone:
Location:
Date Picked Up:
Date Completed: 3-12-03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

# BioTech-Chem Library
## Search Results
## Feedback Form (Optional)

Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

**Mary Hale, Supervisor, 308-4258**
CM-1 Room 1E01

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*Voluntary Results Feedback Form*

- *I am an examiner in Workgroup:* *(Example: 1610)*
- *Relevant prior art found, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

  *Types of relevant prior art found:*
  - ☐ Foreign Patent(s)
  - ☐ Non-Patent Literature
    (journal articles, conference proceedings, new product announcements etc.)
- *Relevant prior art **not found**:*
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Search results were not useful in determining patentability or understanding the invention.

**Other Comments:**

---

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01** or **mary.hale@uspto.gov**

GenCore version 5.1.4_p5_4578


OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 17:41:50 ; Search time 13178 Seconds
(without alignments)
11645.097 Million cell updates/sec

Title: US-10-003-919-3
Perfect score: 5273
Sequence: 1 ctagggcatggcatcccacg.....aattgtgcctttcttaaaaa 5273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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20: em_om:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
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| | 2 | 30.6 | 0.6 | 31 | 6 | BD002934 | BD002934 Gene comp |
| | 3 | 30.6 | 0.6 | 31 | 6 | BD002935 | BD002935 Gene comp |
| | 4 | 30.6 | 0.6 | 31 | 6 | BD002936 | BD002936 Gene comp |
| | 5 | 30.6 | 0.6 | 31 | 6 | BD002937 | BD002937 Gene comp |
| | 6 | 30.6 | 0.6 | 31 | 6 | BD002938 | BD002938 Gene comp |
| | 7 | 30.6 | 0.6 | 31 | 6 | BD002939 | BD002939 Gene comp |
| | 8 | 30.6 | 0.6 | 31 | 6 | BD002940 | BD002940 Gene comp |
| | 9 | 30.6 | 0.6 | 31 | 6 | BD002941 | BD002941 Gene comp |
| | 10 | 30.6 | 0.6 | 31 | 6 | BD002942 | BD002942 Gene comp |
| | 11 | 30.6 | 0.6 | 31 | 6 | BD002943 | BD002943 Gene comp |
| c | 12 | 28.4 | 0.5 | 50 | 6 | AR178318 | AR178318 Sequence |
| c | 13 | 28.4 | 0.5 | 50 | 6 | AX323400 | AX323400 Sequence |
| c | 14 | 25.8 | 0.5 | 50 | 6 | AX057285 | AX057285 Sequence |
| | 15 | 25.4 | 0.5 | 43 | 8 | YSCMTP032 | J01517 Yeast (S.ce |
| | 16 | 24.8 | 0.5 | 30 | 6 | AR208348 | AR208348 Sequence |
| | 17 | 24.8 | 0.5 | 38 | 6 | AX207477 | AX207477 Sequence |
| | 18 | 24.8 | 0.5 | 43 | 8 | YSCMTP031 | J01516 Yeast (S.ce |
| | 19 | 24.4 | 0.5 | 27 | 6 | AX175242 | AX175242 Sequence |
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| c | 21 | 23.6 | 0.4 | 32 | 6 | AR002289 | AR002289 Sequence |
| c | 22 | 23.6 | 0.4 | 32 | 6 | AR053140 | AR053140 Sequence |
| | 23 | 23.4 | 0.4 | 34 | 6 | AR001554 | AR001554 Sequence |
| | 24 | 23.4 | 0.4 | 35 | 6 | AR001553 | AR001553 Sequence |
| | 25 | 23.4 | 0.4 | 36 | 6 | AR001552 | AR001552 Sequence |
| | 26 | 23.4 | 0.4 | 37 | 6 | AR001551 | AR001551 Sequence |
| | 27 | 23.4 | 0.4 | 38 | 6 | AR001550 | AR001550 Sequence |
| | 28 | 23.4 | 0.4 | 39 | 6 | AR001549 | AR001549 Sequence |
| | 29 | 23.4 | 0.4 | 40 | 6 | AR001548 | AR001548 Sequence |
| | 30 | 23.4 | 0.4 | 41 | 6 | AR001547 | AR001547 Sequence |
| | 31 | 23.4 | 0.4 | 42 | 6 | AR001546 | AR001546 Sequence |
| | 32 | 23.4 | 0.4 | 43 | 6 | AR001545 | AR001545 Sequence |
| | 33 | 23.4 | 0.4 | 45 | 6 | AR001543 | AR001543 Sequence |
| c | 34 | 23.4 | 0.4 | 47 | 12 | SYNPRWA | M94403 Artificial |
| c | 35 | 23.4 | 0.4 | 50 | 6 | AX158294 | AX158294 Sequence |
| c | 36 | 23.2 | 0.4 | 33 | 6 | AX183778 | AX183778 Sequence |
| c | 37 | 23 | 0.4 | 43 | 6 | AX484515 | AX484515 Sequence |
| c | 38 | 23 | 0.4 | 45 | 6 | AR083212 | AR083212 Sequence |
| | 39 | 23 | 0.4 | 47 | 6 | AX378317 | AX378317 Sequence |
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ALIGNMENTS

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LOCUS I31473 44 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 385 from patent US 5582979.
ACCESSION I31473
VERSION I31473.1 GI:1822264
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 385 10-DEC-1996;

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  Best Local Similarity   83.3%;  Pred. No. 1e+05;
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Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAA 311
          ||||||||||| ||||||||||||||||  ||  | | ||||||
Db     43 CTCTCTCTCTCTCTCTCTCTCTCTCTCTGCTACTGTAA 2


RESULT 2
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LOCUS       BD002934                 31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002934
VERSION     BD002934.1  GI:18630895
KEYWORDS    JP 2000245487-A/600.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 600 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
            PN   JP 2000245487-A/600
            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
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  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    983 GAGCCTCTCCGAGACATTGTTCCAGCGACTG 1013
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Db      1 GAGCCTCTCCGAGACRTTGTTCCAGCGACTG 31


RESULT 3
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LOCUS       BD002935                 31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002935
VERSION     BD002935.1  GI:18630896
KEYWORDS    JP 2000245487-A/601.
SOURCE      unidentified.
  ORGANISM  unidentified
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REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 601 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
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            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
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BASE COUNT        9 a      7 c      7 g      7 t      1 others
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  Best Local Similarity   96.8%;  Pred. No. 1.1e+05;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1313 GACAAGCCTGTTGTCATCCATTGAAGACAAG 1343
          |||||||||||||||:|||||||||||||||
Db      1 GACAAGCCTGTTGTCRTCCATTGAAGACAAG 31


RESULT 4
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LOCUS       BD002936                 31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002936
VERSION     BD002936.1  GI:18630897
KEYWORDS    JP 2000245487-A/602.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 602 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
            PN   JP 2000245487-A/602
            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
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            FH   Key             Location/Qualifiers
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ORIGIN

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  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1535 GAAAATCCTGCAGCTCATTAAGTCACAGAAA 1565
          |||||||||||||||:|||||||||||||||
Db      1 GAAAATCCTGCAGCTSATTAAGTCACAGAAA 31


RESULT 5
BD002937
LOCUS       BD002937                 31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002937
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VERSION     BD002937.1  GI:18630898
KEYWORDS    JP 2000245487-A/603.
SOURCE      unidentified.
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REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 603 12-SEP-2000;
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COMMENT     OS   Unknown
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            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
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            PC   C12N15/09,C12Q1/68,C12N15/00
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  Best Local Similarity   96.8%;  Pred. No. 1.1e+05;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3464 TCCCAGGACACAGGAGTCAAGGCCCAGTGAC 3494
           |||||||||||||||:|||||||||||||||
Db      1 TCCCAGGACACAGGARTCAAGGCCCAGTGAC 31


RESULT 6
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LOCUS       BD002938                  31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002938
VERSION     BD002938.1  GI:18630899
KEYWORDS    JP 2000245487-A/604.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 604 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
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            PR   27-JAN-1999 US   09/238.402
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Db      1 AACACCGAGCTCCCGYATCACGGCAAGCACC 31


RESULT 7
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LOCUS       BD002939                  31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002939
VERSION     BD002939.1  GI:18630900
KEYWORDS    JP 2000245487-A/605.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 605 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
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            PD   12-SEP-2000
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            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
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Db      1 CCATGCAGTGAAGCCYTCAGTGAGCTGCCAC 31


RESULT 8
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DEFINITION  Gene composition and method.
ACCESSION   BD002940
VERSION     BD002940.1  GI:18630901
KEYWORDS    JP 2000245487-A/606.
SOURCE      unidentified.
  ORGANISM  unidentified
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REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 606 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
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            PD   12-SEP-2000
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            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
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DEFINITION  Gene composition and method.
ACCESSION   BD002941
VERSION     BD002941.1  GI:18630902
KEYWORDS    JP 2000245487-A/607.
SOURCE      unidentified.
  ORGANISM  unidentified
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REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 607 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
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LOCUS       BD002942                  31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002942
VERSION     BD002942.1  GI:18630903
KEYWORDS    JP 2000245487-A/608.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 608 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
            PN   JP 2000245487-A/608
            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
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BASE COUNT        7 a      7 c      8 g      8 t      1 others
ORIGIN

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Db      1 GATCGAACACTCATGRTGTGCCAAGTGCTGT 31


RESULT 11
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LOCUS       BD002943                  31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002943
VERSION     BD002943.1  GI:18630904
KEYWORDS    JP 2000245487-A/609.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 609 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
            PN   JP 2000245487-A/609
            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .31
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      8 c      9 g      8 t      1 others
ORIGIN

  Query Match             0.6%;  Score 30.6;  DB 6;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 1.1e+05;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4722 GCTTTAGCTAAAGTCCCGCGGGTTCCGGCAT 4752
           |||||||||||||||:|||||||||||||||
Db      1 GCTTTAGCTAAAGTCYCGCGGGTTCCGGCAT 31


RESULT 12
AR178318/c
LOCUS       AR178318                  50 bp    DNA     linear   PAT 20-APR-2002
```

```
DEFINITION  Sequence 35 from patent US 6319672.
ACCESSION   AR178318
VERSION     AR178318.1  GI:20219456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: US 6319672-A 35 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       25 a      0 c      25 g      0 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 6;  Length 50;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+05;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
           | | | |||||||||| ||||||||||||||||  ||   | ||| |
Db      49 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4


RESULT 13
AX323400/c
LOCUS       AX323400                 50 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 35 from Patent WO0192511.
ACCESSION   AX323400
VERSION     AX323400.1  GI:18094162
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: WO 0192511-A 35 06-DEC-2001;
            Aventis Pharma (FR)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
BASE COUNT       25 a      0 c      25 g      0 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 6;  Length 50;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+05;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
           | | | |||||||||| ||||||||||||||||  ||   | ||| |
Db      49 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4


RESULT 14
AX057285/c
LOCUS       AX057285                 50 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 16 from Patent WO0075329.
ACCESSION   AX057285
VERSION     AX057285.1  GI:12310031
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Levine,A.J., Mitterer,A., Falkner,F.G., Scheiflinger,F. and
            Dorner,F.
  TITLE     Targeted angiogenesis
  JOURNAL   Patent: WO 0075329-A 16 14-DEC-2000;
            Edwards Lifesciences Corporation (US) ; Baxter Aktiengesellschaft
            (AT)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="annealed oligonucleotide"
BASE COUNT       3 a      16 c      27 g      4 t
ORIGIN

  Query Match             0.5%;  Score 25.8;  DB 6;  Length 50;
  Best Local Similarity   73.3%;  Pred. No. 1.1e+06;
  Matches   33;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    3898 ACCAGCAGACCCCGCCCACCCCGACGCCGCGGCCGCCGCTGCCAG 3942
           | | || | | ||||   | ||| |||||| |||||||| ||||
Db      48 AGCCGCCGCCGCCGCTGCCGCCGCCGCCGCTGCCGCCGCCGCCAG 4


RESULT 15
YSCMTP032
LOCUS       YSCMTP032                43 bp    DNA     linear   PLN 04-AUG-1993
DEFINITION  Yeast (S.cerevisiae) mitochondrial petite mutant excision seq 3,
            right end.
ACCESSION   J01517
VERSION     J01517.1  GI:343850
KEYWORDS    AT-rich region; GC rich region.
SEGMENT     2 of 2
SOURCE      Yeast (Saccharomyces cerevisiae) mitochondrial DNA.
  ORGANISM  Mitochondrion Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   de Zamaroczy,M., Faugeron-Fonty,G. and Bernardi,G.
  TITLE     Excision sequences in the mitochondrial genome of yeast
  JOURNAL   Gene 21 (3), 193-202 (1983)
  MEDLINE   83210931
   PUBMED   6343188
COMMENT     Additional sequences reported in [1], but sequenced in earlier
            papers, appear in separate entries. Excision repeat corresponds to
            bases 11 to 33.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Saccharomyces cerevisiae"
                     /organelle="mitochondrion"
                     /db_xref="taxon:4932"
BASE COUNT       20 a      4 c      4 g      15 t
ORIGIN

  Query Match             0.5%;  Score 25.4;  DB 8;  Length 43;
  Best Local Similarity   82.9%;  Pred. No. 1.3e+06;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    4409 TATAGATAATAATAATATTAATAATAATAATGGCC 4443
           |||  |||||||||||| |||||||||||| | ||
Db       3 TATTATTAATAATAATAATAATAATAATAAAGTCC 37


Search completed: March 12, 2003, 00:54:47
Job time : 13185 secs
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GenCore version 5.1.4_p5_4578


OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 17:32:35 ; Search time 1010 Seconds
(without alignments)
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Title: US-10-003-919-3
Perfect score: 5273
Sequence: 1 ctagggcatggcatcccacg.....aattgtgccttttcttaaaaa 5273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 31.2 | 0.6 | 49 | 13 | AAQ33591 | Microsatellite seq |
| c | 2 | 30.8 | 0.6 | 44 | 18 | AAT65793 | Repeat sequence fr |
| | 3 | 30.6 | 0.6 | 31 | 21 | AAA79230 | Human genomic DNA |
| | 4 | 30.6 | 0.6 | 31 | 21 | AAA79231 | Human genomic DNA |
| | 5 | 30.6 | 0.6 | 31 | 21 | AAA79232 | Human genomic DNA |
| | 6 | 30.6 | 0.6 | 31 | 21 | AAA79233 | Human genomic DNA |
| | 7 | 30.6 | 0.6 | 31 | 21 | AAA79234 | Human genomic DNA |
| | 8 | 30.6 | 0.6 | 31 | 21 | AAA79235 | Human genomic DNA |
| | 9 | 30.6 | 0.6 | 31 | 21 | AAA79236 | Human genomic DNA |
| | 10 | 30.6 | 0.6 | 31 | 21 | AAA79237 | Human genomic DNA |
| | 11 | 30.6 | 0.6 | 31 | 21 | AAA79238 | Human genomic DNA |
| | 12 | 30.6 | 0.6 | 31 | 21 | AAA79239 | Human genomic DNA |
| c | 13 | 28.4 | 0.5 | 48 | 13 | AAQ33615 | Microsatellite seq |
| c | 14 | 28.4 | 0.5 | 50 | 24 | AAS21107 | (GA)25 DNA purific |
| c | 15 | 28.2 | 0.5 | 50 | 21 | AAC31611 | Human secreted pro |
| c | 16 | 28 | 0.5 | 44 | 13 | AAQ33577 | Microsatellite seq |
| c | 17 | 28 | 0.5 | 47 | 20 | AAX30238 | PCR amplification |
| | 18 | 27.2 | 0.5 | 32 | 22 | AAD19287 | Mammalian IL-12 p4 |
| | 19 | 26.8 | 0.5 | 38 | 23 | AAS13726 | Simple sequence re |
| | 20 | 26.8 | 0.5 | 48 | 20 | AAX30240 | PCR amplification |
| c | 21 | 26.4 | 0.5 | 36 | 13 | AAQ33540 | Microsatellite seq |
| c | 22 | 26.4 | 0.5 | 36 | 13 | AAQ33597 | Microsatellite seq |
| | 23 | 26.4 | 0.5 | 38 | 24 | AAL45123 | Oligonucleotide sy |
| c | 24 | 26 | 0.5 | 49 | 13 | AAQ33523 | Sequence of micros |
| | 25 | 25.8 | 0.5 | 42 | 18 | AAT47461 | Foldback triplex f |
| c | 26 | 25.6 | 0.5 | 32 | 13 | AAQ33551 | Microsatellite seq |
| c | 27 | 25.6 | 0.5 | 33 | 13 | AAQ33565 | Microsatellite seq |
| c | 28 | 25.6 | 0.5 | 33 | 21 | AAA74332 | Loblolly pine SSR |
| c | 29 | 25.6 | 0.5 | 36 | 21 | AAA74333 | Loblolly pine SSR |
| c | 30 | 25.6 | 0.5 | 48 | 21 | AAA09913 | Primer Aco2P2 for |
| | 31 | 25.2 | 0.5 | 30 | 23 | AAS13774 | Simple sequence re |
| c | 32 | 25.2 | 0.5 | 30 | 24 | AAL42352 | Novel sand pear mi |
| c | 33 | 25.2 | 0.5 | 31 | 13 | AAQ33543 | Microsatellite seq |
| | 34 | 24.8 | 0.5 | 30 | 23 | AAS13725 | Simple sequence re |
| c | 35 | 24.8 | 0.5 | 30 | 23 | AAS13785 | Simple sequence re |
| | 36 | 24.8 | 0.5 | 38 | 22 | AAH46872 | B. napus turgor ge |
| | 37 | 24.4 | 0.5 | 27 | 22 | AAH46006 | Synthetic oligonuc |
| c | 38 | 24.4 | 0.5 | 30 | 21 | ABN81201 | Litopenaeus vannem |
| c | 39 | 24.4 | 0.5 | 36 | 13 | AAQ30397 | Oligomer LAP322 fo |
| | 40 | 24.4 | 0.5 | 40 | 18 | AAT47475 | Foldback triplex f |
| c | 41 | 24.2 | 0.5 | 45 | 13 | AAQ33517 | Sequence of micros |
| | 42 | 23.8 | 0.5 | 29 | 22 | AAD19288 | Mammalian IL-12 p4 |
| c | 43 | 23.8 | 0.5 | 44 | 18 | AAT61246 | Human antibody hea |
| | 44 | 23.4 | 0.4 | 34 | 15 | AAQ70852 | Foldback triplex-f |
| | 45 | 23.4 | 0.4 | 35 | 15 | AAQ70851 | Foldback triplex-f |

ALIGNMENTS

RESULT 1
AAQ33591/c
ID AAQ33591 standard; DNA; 49 BP.
XX
AC AAQ33591;
XX
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone AGLA2B5.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX

```
PS   Table 7; Page 165; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised. Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000. The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM). The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 49 BP; 33 A; 0 C; 16 G; 0 U; 0 other;

  Query Match             0.6%;  Score 31.2;  DB 13;  Length 49;
  Best Local Similarity   81.8%;  Pred. No. 8e+02;
  Matches   36;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    266 CCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
          | | ||||||||||||||||||||||||||  |||  ||| | |
Db     48 CTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTTTTTTTTTTT 5


RESULT 2
AAT65793/c
ID   AAT65793 standard; DNA; 44 BP.
XX
AC   AAT65793;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Repeat sequence from polymorphic marker clone Mfd122.
XX
KW   Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW   PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW   linkage analysis; genetic disease; animal; plant; breeding; locus;
KW   hybridisation; chromosome; ds.
XX
OS   Homo sapiens.
XX
PN   US5582979-A.
XX
PD   10-DEC-1996.
XX
PF   21-APR-1989;   89US-0341562.
XX
PR   05-SEP-1991;   91US-0754351.
PR   21-APR-1989;   89US-0341562.
PR   04-APR-1994;   94US-0222177.
XX
PA   (MARS-) MARSHFIELD CLINIC.
XX
PI   Weber JL;
XX
DR   WPI; 1997-042299/04.
XX
PT   Detection of polymorphic genetic markers of the form
PT   (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX
PS   Disclosure; Column 13-14; 186pp; English.
XX
CC   The invention relates to the isolation of polymorphic repeat sequences
CC   having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC   markers.  Primers based on these sequences can be used to detect these
CC   repeats, especially for use in e.g paternity or maternity testing,
CC   human genetic analysis such as linkage analysis of genetic disease,
CC   commercial animal or plant breeding or pedigree analysis.  Clones
CC   containing the repeat sequences were isolated by hybridisation of
CC   chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC   probe.  Over 100 repeat blocks were isolated. The inserts from the
CC   clones were amplified by primers AAT65798-T66047.  Those clones where the
CC   repeat sequence has been determined are shown in AAT65704-797.  This
CC   repeat sequence is from the marker clone Mdf122 which contains the
CC   repeat sequence having the formula: TTTACAGTAG(CA)17
XX
SQ   Sequence 44 BP; 20 A; 2 C; 18 G; 4 T; 0 other;

  Query Match             0.6%;  Score 30.8;  DB 18;  Length 44;
  Best Local Similarity   83.3%;  Pred. No. 9.5e+02;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAA 311
          |||||||||| ||||||||||||||||  ||  | | ||||||
Db     43 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGCTACTGTAA 2


RESULT 3
AAA79230
ID   AAA79230 standard; DNA; 31 BP.
XX
AC   AAA79230;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:600.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
```

```
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 5 A; 10 C; 8 G; 7 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     983 GAGCCTCTCCGAGACATTGTTCCAGCGACTG 1013
           ||||||||||||||||:||||||||||||||
Db       1 GAGCCTCTCCGAGACRTTGTTCCAGCGACTG 31


RESULT 4
AAA79231
ID   AAA79231 standard; DNA; 31 BP.
XX
AC   AAA79231;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:601.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 9 A; 7 C; 7 G; 7 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1313 GACAAGCCTGTTGTCATCCATTGAAGACAAG 1343
           |||||||||||||||:|||||||||||||||
Db       1 GACAAGCCTGTTGTCRTCCATTGAAGACAAG 31


RESULT 5
AAA79232
ID   AAA79232 standard; DNA; 31 BP.
XX
AC   AAA79232;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:602.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 13 A; 6 C; 5 G; 6 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy   1535 GAAAATCCTGCAGCTCATTAAGTCACAGAAA 1565
          |||||||||||||||:|||||||||||||||
Db      1 GAAAATCCTGCAGCTSATTAAGTCACAGAAA 31
```

RESULT 6
AAA79233
ID  AAA79233 standard; DNA; 31 BP.
XX
AC  AAA79233;
XX
DT  20-NOV-2000  (first entry)
XX
DE  Human genomic DNA polymorphic site sequence tag SEQ ID NO:603.
XX
KW  Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW  probe; hybridisation; polymorphic site; forensic; paternity testing;
KW  medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS  Homo sapiens.
XX
PN  EP1024200-A2.
XX
PD  02-AUG-2000.
XX
PF  26-JAN-2000; 2000EP-0250023.
XX
PR  27-JAN-1999;  99US-0238402.
XX
PA  (AFFY-) AFFYMETRIX INC.
XX
PI  Patil N,  Shah N,  Warrigton JA;
XX
DR  WPI; 2000-500198/45.
XX
PT  Human genomic polymorphic nucleic acid segments, allele specific
PT  primers and probes, and methods of analysis, useful for e.g. forensics,
PT  paternity testing, genetic mapping,  -
XX
PS  Claim 1; Page 22; 141pp; English.
XX
CC  The present invention describes a nucleic acid segment of 10-100
CC  contiguous bases chosen from one of 632 fragments (AAA78631 to
CC  AAA79262), where the segment comprises a polymorphic site or an
CC  immediately adjacent base, or the complement of the segment. Also
CC  described are: (1) an allele-specific oligonucleotide that hybridises to
CC  a segment of the novelty; (2) an isolated nucleic acid comprising a
CC  sequence of the novelty where the polymorphic site within the sequence is
CC  occupied by a base other than the reference base indicated in the
CC  specification; and (3) analysing a nucleic acid, comprising obtaining a
CC  nucleic acid from an individual, and determining a base occupying any one
CC  of the polymorphic sites of the novelty. The nucleic acid segments and
CC  method can be used to analyse an individuals nucleic acid sequences for
CC  the presence of polymorphisms. The method can also be used to test for a
CC  disease phenotype and correlate the presence of the phenotype with a
CC  particular polymorphism. The presence of polymorphic sites are useful
CC  for, e.g. forensics, paternity testing, correlation of polymorphisms
CC  with phenotypic traits and for genetic mapping of phenotypic traits.
CC  AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC  fragments containing polymorphic sites. The base occupying the
CC  polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ  Sequence 31 BP; 9 A; 10 C; 8 G; 3 T; 1 other;

```
  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3464 TCCCAGGACACAGGAGTCAAGGCCCAGTGAC 3494
          |||||||||||||||:|||||||||||||||
Db      1 TCCCAGGACACAGGARTCAAGGCCCAGTGAC 31
```

RESULT 7
AAA79234
ID  AAA79234 standard; DNA; 31 BP.
XX
AC  AAA79234;
XX
DT  20-NOV-2000  (first entry)
XX
DE  Human genomic DNA polymorphic site sequence tag SEQ ID NO:604.
XX
KW  Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW  probe; hybridisation; polymorphic site; forensic; paternity testing;
KW  medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS  Homo sapiens.
XX
PN  EP1024200-A2.
XX
PD  02-AUG-2000.
XX
PF  26-JAN-2000; 2000EP-0250023.
XX
PR  27-JAN-1999;  99US-0238402.
XX
PA  (AFFY-) AFFYMETRIX INC.
XX
PI  Patil N,  Shah N,  Warrigton JA;
XX
DR  WPI; 2000-500198/45.
XX
PT  Human genomic polymorphic nucleic acid segments, allele specific
PT  primers and probes, and methods of analysis, useful for e.g. forensics,
PT  paternity testing, genetic mapping,  -
XX
PS  Claim 1; Page 22; 141pp; English.
XX
CC  The present invention describes a nucleic acid segment of 10-100
CC  contiguous bases chosen from one of 632 fragments (AAA78631 to
CC  AAA79262), where the segment comprises a polymorphic site or an
CC  immediately adjacent base, or the complement of the segment. Also
CC  described are: (1) an allele-specific oligonucleotide that hybridises to
CC  a segment of the novelty; (2) an isolated nucleic acid comprising a
CC  sequence of the novelty where the polymorphic site within the sequence is
CC  occupied by a base other than the reference base indicated in the
CC  specification; and (3) analysing a nucleic acid, comprising obtaining a
CC  nucleic acid from an individual, and determining a base occupying any one
CC  of the polymorphic sites of the novelty. The nucleic acid segments and
CC  method can be used to analyse an individuals nucleic acid sequences for
CC  the presence of polymorphisms. The method can also be used to test for a
CC  disease phenotype and correlate the presence of the phenotype with a
CC  particular polymorphism. The presence of polymorphic sites are useful
CC  for, e.g. forensics, paternity testing, correlation of polymorphisms
CC  with phenotypic traits and for genetic mapping of phenotypic traits.
CC  AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC  fragments containing polymorphic sites. The base occupying the
CC  polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ  Sequence 31 BP; 9 A; 13 C; 6 G; 2 T; 1 other;

```
  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3999 AACACCGAGCTCCCGCATCACGGCAAGCACC 4029
          |||||||||||||||:|||||||||||||||
Db      1 AACACCGAGCTCCCGYATCACGGCAAGCACC 31
```

RESULT 8
AAA79235
ID  AAA79235 standard; DNA; 31 BP.
XX
AC  AAA79235;

```
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:605.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 7 A; 10 C; 8 G; 5 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4069 CCATGCAGTGAAGCCCTCAGTGAGCTGCCAC 4099
          |||||||||||||||:|||||||||||||||
Db      1 CCATGCAGTGAAGCCYTCAGTGAGCTGCCAC 31


RESULT 9
AAA79236
ID   AAA79236 standard; DNA; 31 BP.
XX
AC   AAA79236;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:606.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 2 A; 9 C; 9 G; 10 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4310 TCTGGGTCCCCAGCTCGCTCTTGGTACTTGG 4340
          |||||||||||||||:|||||||||||||||
Db      1 TCTGGGTCCCCAGCTYGCTCTTGGTACTTGG 31


RESULT 10
AAA79237
ID   AAA79237 standard; DNA; 31 BP.
XX
AC   AAA79237;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:607.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
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XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 4 A; 9 C; 11 G; 6 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4339 GGGACCCCAGTGCCTCGTTGAGGGCGCCATT 4369
            |||||||||||||||:|||||||||||||||
Db      1 GGGACCCCAGTGCCTYGTTGAGGGCGCCATT 31


RESULT 11
AAA79238
ID   AAA79238 standard; DNA; 31 BP.
XX
AC   AAA79238;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:608.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 7 A; 7 C; 8 G; 8 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4449 GATCGAACACTCATGATGTGCCAAGTGCTGT 4479
            |||||||||||||||:|||||||||||||||
Db      1 GATCGAACACTCATGRTGTGCCAAGTGCTGT 31


RESULT 12
AAA79239
ID   AAA79239 standard; DNA; 31 BP.
XX
AC   AAA79239;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:609.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
KW   probe; hybridisation; polymorphic site; forensic; paternity testing;
KW   medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-0250023.
XX
PR   27-JAN-1999;   99US-0238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
```

```
XX
PI   Patil N,  Shah N,  Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific
PT   primers and probes, and methods of analysis, useful for e.g. forensics,
PT   paternity testing, genetic mapping,  -
XX
PS   Claim 1; Page 22; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to
CC   AAA79262), where the segment comprises a polymorphic site or an
CC   immediately adjacent base, or the complement of the segment. Also
CC   described are: (1) an allele-specific oligonucleotide that hybridises to
CC   a segment of the novelty; (2) an isolated nucleic acid comprising a
CC   sequence of the novelty where the polymorphic site within the sequence is
CC   occupied by a base other than the reference base indicated in the
CC   specification; and (3) analysing a nucleic acid, comprising obtaining a
CC   nucleic acid from an individual, and determining a base occupying any one
CC   of the polymorphic sites of the novelty. The nucleic acid segments and
CC   method can be used to analyse an individuals nucleic acid sequences for
CC   the presence of polymorphisms. The method can also be used to test for a
CC   disease phenotype and correlate the presence of the phenotype with a
CC   particular polymorphism. The presence of polymorphic sites are useful
CC   for, e.g. forensics, paternity testing, correlation of polymorphisms
CC   with phenotypic traits and for genetic mapping of phenotypic traits.
CC   AAA78631 to AAA79262 represent sequence tags of human genomic DNA
CC   fragments containing polymorphic sites. The base occupying the
CC   polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
SQ   Sequence 31 BP; 5 A; 8 C; 9 G; 8 T; 1 other;

  Query Match             0.6%;  Score 30.6;  DB 21;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 9.1e+02;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    4722 GCTTTAGCTAAAGTCCCGCGGGTTCCGGCAT 4752
           |||||||||||||||:|||||||||||||||
Db       1 GCTTTAGCTAAAGTCYCGCGGGTTCCGGCAT 31


RESULT 13
AAQ33615/c
ID   AAQ33615 standard; DNA; 48 BP.
XX
AC   AAQ33615;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone AGLA33.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 175; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 48 BP; 24 A; 0 C; 24 G; 0 U; 0 other;

  Query Match             0.5%;  Score 28.4;  DB 13;  Length 48;
  Best Local Similarity   76.1%;  Pred. No. 3.8e+03;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
          | | | |||||||||| ||||||||||||||  ||   | ||| |
Db     48 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3


RESULT 14
AAS21107/c
ID   AAS21107 standard; DNA; 50 BP.
XX
AC   AAS21107;
XX
DT   20-MAR-2002  (first entry)
XX
DE   (GA)25 DNA purification oligonucleotide.
XX
KW   ss; DNA purification; triple helix; plasmid purification.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   repeat_region   1..50
FT                   /*tag= a
FT                   /rpt_type= "TANDEM"
FT   repeat_unit     1..2
FT                   /*tag= b
FT                   /note= "GA repeat type"
XX
PN   WO200192511-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US17122.
XX
PR   26-MAY-2000; 2000US-0580923.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Crouzet J,  Scherman D,  Wils P,  Blanche F,  Cameron B;
XX
DR   WPI; 2002-097772/13.
XX
PT   Purifying double-stranded (ds) DNA from a solution containing dsDNA and
PT   other components, comprises passing the solution through a support
PT   comprising a covalently coupled oligonucleotide able to form a triple
PT   helix with the dsDNA  -
XX
```

PS Example 7; Page 20; 40pp; English.
XX
CC This invention comprises a method of purifying double-stranded DNA from
CC a solution containing the double-stranded DNA mixed with other
CC components, comprising passing the solution through a support comprising
CC a covalently coupled oligonucleotide capable of forming a triple helix
CC with the double-stranded DNA by hybridisation with a specific sequence
CC present in the double-stranded DNA. The method is useful for purifying
CC double-stranded DNA contained in a solution and mixed with other
CC components. The new method is a simple, rapid and effective method for
CC DNA purification, and makes it possible to obtain especially high
CC purities with high yields. The method enables DNA to be purified from
CC complex mixtures comprising other nucleic acids, proteins, endotoxins,
CC nucleases and the like. The supports may be readily recycled, and the
CC DNAs obtained display improved properties to pharmaceutical safety.
CC Further, the method entails only one step contrary to prior art.
CC The present sequence represents a DNA sequence contained within the
CC plasmid pXL2726. This sequence is used for purification of this
CC plasmid using the method of the invention.
XX
SQ Sequence 50 BP; 25 A; 0 C; 25 G; 0 U; 0 other;

Query Match 0.5%; Score 28.4; DB 24; Length 50;
Best Local Similarity 76.1%; Pred. No. 3.8e+03;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
|| | | |||||||||| |||||||||||||||| || | ||| |
Db 49 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4

RESULT 15
AAC31611/c
ID AAC31611 standard; cDNA; 50 BP.
XX
AC AAC31611;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 35686.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 35686; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 50 BP; 21 A; 4 C; 19 G; 3 T; 3 other;

Query Match 0.5%; Score 28.2; DB 21; Length 50;
Best Local Similarity 81.1%; Pred. No. 4.3e+03;
Matches 30; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 269 CCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTT 305
|||||||||||||||||||| ||||| | || | : |
Db 43 CCTCTCTCTCTTTCTCTCTCCCTCTCCTTCTNGNYCT 7

Search completed: March 11, 2003, 21:11:19
Job time : 1015 secs

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 20:53:31 ; Search time 164 Seconds
(without alignments)
9860.406 Million cell updates/sec

Title: US-10-003-919-3
Perfect score: 5273
Sequence: 1 ctagggcatggcatcccacg.....aattgtgcctttcttaaaaa 5273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 30.8 | 0.6 | 44 | 1 | US-08-222-177A-385 | Sequence 385, App |
| c | 2 | 28.4 | 0.5 | 50 | 4 | US-09-580-923-35 | Sequence 35, Appl |
| c | 3 | 28 | 0.5 | 47 | 3 | US-08-933-358-18 | Sequence 18, Appl |
| | 4 | 26.8 | 0.5 | 48 | 3 | US-08-933-358-20 | Sequence 20, Appl |
| c | 5 | 25 | 0.5 | 47 | 4 | US-09-641-638-934 | Sequence 934, App |
| c | 6 | 25 | 0.5 | 47 | 4 | US-09-641-638-935 | Sequence 935, App |
| | 7 | 24.8 | 0.5 | 30 | 4 | US-09-281-481A-4 | Sequence 4, Appli |
| | 8 | 24.4 | 0.5 | 28 | 4 | US-09-281-481A-2 | Sequence 2, Appli |
| c | 9 | 23.6 | 0.4 | 32 | 1 | US-08-469-802B-28 | Sequence 28, Appl |
| c | 10 | 23.6 | 0.4 | 32 | 2 | US-08-267-803B-46 | Sequence 46, Appl |
| | 11 | 23.4 | 0.4 | 34 | 1 | US-08-418-123A-15 | Sequence 15, Appl |
| | 12 | 23.4 | 0.4 | 35 | 1 | US-08-418-123A-14 | Sequence 14, Appl |
| | 13 | 23.4 | 0.4 | 36 | 1 | US-08-418-123A-13 | Sequence 13, Appl |
| | 14 | 23.4 | 0.4 | 37 | 1 | US-08-418-123A-12 | Sequence 12, Appl |
| | 15 | 23.4 | 0.4 | 38 | 1 | US-08-418-123A-11 | Sequence 11, Appl |
| | 16 | 23.4 | 0.4 | 39 | 1 | US-08-418-123A-10 | Sequence 10, Appl |
| | 17 | 23.4 | 0.4 | 40 | 1 | US-08-418-123A-9 | Sequence 9, Appli |
| | 18 | 23.4 | 0.4 | 41 | 1 | US-08-418-123A-8 | Sequence 8, Appli |
| | 19 | 23.4 | 0.4 | 42 | 1 | US-08-418-123A-7 | Sequence 7, Appli |
| | 20 | 23.4 | 0.4 | 43 | 1 | US-08-418-123A-6 | Sequence 6, Appli |
| | 21 | 23.4 | 0.4 | 45 | 1 | US-08-418-123A-4 | Sequence 4, Appli |
| c | 22 | 23 | 0.4 | 45 | 2 | US-08-495-695B-19 | Sequence 19, Appl |
| c | 23 | 23 | 0.4 | 45 | 5 | PCT-US94-14436-19 | Sequence 19, Appl |
| c | 24 | 22.6 | 0.4 | 48 | 2 | US-08-418-848A-23 | Sequence 23, Appl |
| c | 25 | 22.4 | 0.4 | 24 | 2 | US-08-808-474A-8 | Sequence 8, Appli |
| | 26 | 22.4 | 0.4 | 24 | 2 | US-08-808-474A-9 | Sequence 9, Appli |
| | 27 | 22.4 | 0.4 | 24 | 2 | US-08-808-474A-10 | Sequence 10, Appl |
| c | 28 | 22.4 | 0.4 | 24 | 2 | US-08-808-474A-11 | Sequence 11, Appl |
| c | 29 | 22.4 | 0.4 | 24 | 4 | US-09-235-614-8 | Sequence 8, Appli |
| | 30 | 22.4 | 0.4 | 24 | 4 | US-09-235-614-9 | Sequence 9, Appli |
| | 31 | 22.4 | 0.4 | 24 | 4 | US-09-235-614-10 | Sequence 10, Appl |
| c | 32 | 22.4 | 0.4 | 24 | 4 | US-09-235-614-11 | Sequence 11, Appl |
| | 33 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-1 | Sequence 1, Appli |
| c | 34 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-2 | Sequence 2, Appli |
| | 35 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-3 | Sequence 3, Appli |
| | 36 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-4 | Sequence 4, Appli |
| c | 37 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-5 | Sequence 5, Appli |
| | 38 | 22.4 | 0.4 | 24 | 4 | US-09-487-130-6 | Sequence 6, Appli |
| c | 39 | 22.4 | 0.4 | 33 | 1 | US-08-068-747-7 | Sequence 7, Appli |
| | 40 | 22.4 | 0.4 | 33 | 1 | US-08-418-123A-16 | Sequence 16, Appl |
| | 41 | 22.4 | 0.4 | 43 | 1 | US-08-418-123A-5 | Sequence 5, Appli |
| c | 42 | 22.4 | 0.4 | 50 | 3 | US-08-846-020A-6 | Sequence 6, Appli |
| c | 43 | 22.4 | 0.4 | 50 | 4 | US-09-617-871-6 | Sequence 6, Appli |
| | 44 | 22.2 | 0.4 | 36 | 1 | US-08-004-800-16 | Sequence 16, Appl |
| | 45 | 22.2 | 0.4 | 36 | 1 | US-08-413-813-16 | Sequence 16, Appl |

ALIGNMENTS

RESULT 1
US-08-222-177A-385/c
; Sequence 385, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfdl22rs
US-08-222-177A-385

Query Match 0.6%; Score 30.8; DB 1; Length 44;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAA 311
          |||||||||| |||||||||||||||  ||  | | ||||||
Db     43 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGCTACTGTAA 2
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RESULT 2
US-09-580-923-35/c
; Sequence 35, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wils, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-35

Query Match 0.5%; Score 28.4; DB 4; Length 50;
Best Local Similarity 76.1%; Pred. No. 2.9e+02;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy    264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
          | | | |||||||||| ||||||||||||||  ||   | ||| |
Db     49 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4
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RESULT 3
US-08-933-358-18/c
; Sequence 18, Application US/08933358
; Patent No. 6013444
; GENERAL INFORMATION:
; APPLICANT: Dau, Peter C.
; APPLICANT: Liu, Debang
; TITLE OF INVENTION: DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR
; TITLE OF INVENTION: ELECTROPHORESIS
; FILE REFERENCE: 434001aa
; CURRENT APPLICATION NUMBER: US/08/933,358
; CURRENT FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PRIMER SEQUENCE
US-08-933-358-18

Query Match 0.5%; Score 28; DB 3; Length 47;
Best Local Similarity 77.3%; Pred. No. 3.6e+02;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy    272 CTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAATGAG 315
          |||| ||||||| ||| ||| |||| |||  ||||| | | |||
Db     46 CTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTGAAGAG 3
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RESULT 4
US-08-933-358-20
; Sequence 20, Application US/08933358
; Patent No. 6013444
; GENERAL INFORMATION:
; APPLICANT: Dau, Peter C.
; APPLICANT: Liu, Debang
; TITLE OF INVENTION: DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR
; TITLE OF INVENTION: ELECTROPHORESIS
; FILE REFERENCE: 434001aa
; CURRENT APPLICATION NUMBER: US/08/933,358
; CURRENT FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PRIMER SEQUENCE
US-08-933-358-20

Query Match 0.5%; Score 26.8; DB 3; Length 48;
Best Local Similarity 73.9%; Pred. No. 7.4e+02;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy    267 CCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAAT 312
          | | || || ||||||| ||| ||| |||| |||  ||||| | ||
Db      3 CTCTTCACTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCATT 48
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RESULT 5
US-09-641-638-934/c
; Sequence 934, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 934
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-836-237 : polymorphic base A or G
US-09-641-638-934

Query Match 0.5%; Score 25; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 28; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy    271 TCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTT 305
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Db      43 TCTCTCTCTCTCTCTCAYTCGCTCGCTTGCTCT 9


RESULT 6
US-09-641-638-935/c
; Sequence 935, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
;  TITLE OF INVENTION:  GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
;  FILE REFERENCE:  GENSET.051CP1
;  CURRENT APPLICATION NUMBER: US/09/641,638
;  CURRENT FILING DATE:  2000-08-16
;  PRIOR APPLICATION NUMBER:  US 09/502,330
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  US 60/133,200
;  PRIOR FILING DATE:  1999-05-07
;  PRIOR APPLICATION NUMBER:  US 09/275,267
;  PRIOR FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER:  US 60/119,917
;  PRIOR FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS:  1304
;  SOFTWARE:  Patent.pm
; SEQ ID NO 935
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 12-836-238 : polymorphic base A or T
US-09-641-638-935

  Query Match             0.5%;  Score 25;  DB 4;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   28;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     271 TCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTT 305
           ||||||||| |||||||: || || ||||| | |
Db      42 TCTCTCTCTCTCTCTCWTTCGCTCGCTTGCTCT 8


RESULT 7
US-09-281-481A-4
; Sequence 4, Application US/09281481A
; Patent No. 6383747
;  GENERAL INFORMATION:
;     APPLICANT:  DAWKINS, Roger L. and ABRAHAM, Lawrence J.
;     TITLE OF INVENTION:  GENETIC ANALYSIS
;     NUMBER OF SEQUENCES:  22
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY SCOTT MURPHY & PRESSER
;       STREET:  400 GARDEN CITY PLAZA
;       CITY:  GARDEN CITY
;       STATE:  NEW YORK
;       COUNTRY:  UNITED STATES OF AMERICA
;       ZIP:  11530-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/281,481A
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/893,971
;       FILING DATE:  16-JUL-1997
;       APPLICATION NUMBER:  US 232,229
;       FILING DATE:  29-APR-1994
;       APPLICATION NUMBER:  PK9279 (AU)
;       FILING DATE:  01-NOV-1991
;       APPLICATION NUMBER:  PCT/AU92/00583
;       FILING DATE:  30-OCT-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DIGIGLIO, FRANK S
;       REFERENCE/DOCKET NUMBER:  9279
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  +516 742 4343
;       TELEFAX:  +516 742 4366
;  INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-09-281-481A-4

  Query Match             0.5%;  Score 24.8;  DB 4;  Length 30;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+03;
  Matches   26;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     268 CCCTCTCTCTCTTTCTCTCTCTCTCT 295
           | ||||||||| ||||||||||||||
Db       2 CTCTCTCTCTCTCTCTCTCTCTCTCT 29


RESULT 8
US-09-281-481A-2
; Sequence 2, Application US/09281481A
; Patent No. 6383747
;  GENERAL INFORMATION:
;     APPLICANT:  DAWKINS, Roger L. and ABRAHAM, Lawrence J.
;     TITLE OF INVENTION:  GENETIC ANALYSIS
;     NUMBER OF SEQUENCES:  22
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY SCOTT MURPHY & PRESSER
;       STREET:  400 GARDEN CITY PLAZA
;       CITY:  GARDEN CITY
;       STATE:  NEW YORK
;       COUNTRY:  UNITED STATES OF AMERICA
;       ZIP:  11530-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/281,481A
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/893,971
;       FILING DATE:  16-JUL-1997
;       APPLICATION NUMBER:  US 232,229
;       FILING DATE:  29-APR-1994
;       APPLICATION NUMBER:  PK9279 (AU)
;       FILING DATE:  01-NOV-1991
;       APPLICATION NUMBER:  PCT/AU92/00583
;       FILING DATE:  30-OCT-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DIGIGLIO, FRANK S
;       REFERENCE/DOCKET NUMBER:  9279
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  +516 742 4343
;       TELEFAX:  +516 742 4366
;  INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-281-481A-2

  Query Match              0.5%;  Score 24.4;  DB 4;  Length 28;
  Best Local Similarity   96.2%;  Pred. No. 2.3e+03;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTCT 295
          ||||||||||  ||||||||||||||||
Db      2 CTCTCTCTCTCTCTCTCTCTCTCTCT 27


RESULT 9
US-08-469-802B-28/c
; Sequence 28, Application US/08469802B
; Patent No. 5741645
;  GENERAL INFORMATION:
;    APPLICANT:  Orr, Harry T.
;    APPLICANT:  Ranum, Laura P.W.
;    APPLICANT:  Chung, Ming-yi
;    APPLICANT:  Zoghbi, Huda Y.
;    TITLE OF INVENTION:  Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
;    TITLE OF INVENTION:  Type 1 and Method for Diagnosis
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  119 No. 5741645th Fourth Street, Suite 203
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,802B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00030101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1225
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-469-802B-28

  Query Match              0.4%;  Score 23.6;  DB 1;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 4.1e+03;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTTGCT 299
          ||||||||||  ||||||||||| || | ||
Db     31 CTCTCTCTCTCTCTCTCTCTGTCATTCT 2


RESULT 10
US-08-267-803B-46/c
; Sequence 46, Application US/08267803B
; Patent No. 5834183
;  GENERAL INFORMATION:
;    APPLICANT:  Orr, Harry T.
;    APPLICANT:  Ranum, Laura P.W.
;    APPLICANT:  Chung, Ming-yi
;    APPLICANT:  Zoghbi, Huda Y.
;    TITLE OF INVENTION:  Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
;    TITLE OF INVENTION:  Type 1 and Method for Diagnosis
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/267,803B
;      FILING DATE:  28-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCormack, Myra H.
;      REGISTRATION NUMBER:  36,602
;      REFERENCE/DOCKET NUMBER:  110.00030120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-267-803B-46

  Query Match              0.4%;  Score 23.6;  DB 2;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 4.1e+03;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTTGCT 299
          ||||||||||  ||||||||||| || | ||
Db     31 CTCTCTCTCTCTCTCTCTCTGTCATTCT 2


RESULT 11
US-08-418-123A-15
; Sequence 15, Application US/08418123A
; Patent No. 5739308
;  GENERAL INFORMATION:
;    APPLICANT:  Kandimalla, Ekambar R.
;    APPLICANT:  Agrawal, Sudhir
;    TITLE OF INVENTION:  Integrated Oligonucleotides
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 7.0 for Windows 95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/418,123A
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;      FILING DATE:  April 6, 1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greenfield, Michael S.
;      REGISTRATION NUMBER:  37,142
;      REFERENCE/DOCKET NUMBER:  93,000-E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/715-1000
;      TELEFAX:  312/715-1234
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-418-123A-15

  Query Match             0.4%;  Score 23.4;  DB 1;  Length 34;
  Best Local Similarity   81.8%;  Pred. No. 4.7e+03;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    263 CCCCCCCCTCTCTCTCTTTCTCTCTCTCTCT 295
          | | ||| |||||||| |||||||| ||||||
Db      2 CGCACCCATCTCTCTCCTTCTCTCTTCCTCTCT 34


RESULT 12
US-08-418-123A-14
; Sequence 14, Application US/08418123A
; Patent No. 5739308
;  GENERAL INFORMATION:
;    APPLICANT:  Kandimalla, Ekambar R.
;    APPLICANT:  Agrawal, Sudhir
;    TITLE OF INVENTION:  Integrated Oligonucleotides
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 7.0 for Windows 95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/418,123A
;      FILING DATE:  April 6, 1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greenfield, Michael S.
;      REGISTRATION NUMBER:  37,142
;      REFERENCE/DOCKET NUMBER:  93,000-E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/715-1000
;      TELEFAX:  312/715-1234
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-418-123A-14

  Query Match             0.4%;  Score 23.4;  DB 1;  Length 35;
  Best Local Similarity   81.8%;  Pred. No. 4.8e+03;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    263 CCCCCCCCTCTCTCTCTTTCTCTCTCTCTCT 295
          | | ||| |||||||| |||||||| ||||||
Db      2 CGCACCCATCTCTCTCCTTCTCTCTTCCTCTCT 34


RESULT 13
US-08-418-123A-13
; Sequence 13, Application US/08418123A
; Patent No. 5739308
;  GENERAL INFORMATION:
;    APPLICANT:  Kandimalla, Ekambar R.
;    APPLICANT:  Agrawal, Sudhir
;    TITLE OF INVENTION:  Integrated Oligonucleotides
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 7.0 for Windows 95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/418,123A
;      FILING DATE:  April 6, 1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greenfield, Michael S.
;      REGISTRATION NUMBER:  37,142
;      REFERENCE/DOCKET NUMBER:  93,000-E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/715-1000
;      TELEFAX:  312/715-1234
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-418-123A-13

  Query Match             0.4%;  Score 23.4;  DB 1;  Length 36;
  Best Local Similarity   81.8%;  Pred. No. 4.9e+03;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    263 CCCCCCCCTCTCTCTCTTTCTCTCTCTCTCT 295
          | | ||| |||||||| |||||||| ||||||
Db      2 CGCACCCATCTCTCTCCTTCTCTCTTCCTCTCT 34


RESULT 14
US-08-418-123A-12
; Sequence 12, Application US/08418123A
; Patent No. 5739308
;  GENERAL INFORMATION:
;    APPLICANT:  Kandimalla, Ekambar R.
;    APPLICANT:  Agrawal, Sudhir
;    TITLE OF INVENTION:  Integrated Oligonucleotides
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
```

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;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 7.0 for Windows 95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/418,123A
;      FILING DATE:  April 6, 1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greenfield, Michael S.
;      REGISTRATION NUMBER:  37,142
;      REFERENCE/DOCKET NUMBER:  93,000-E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/715-1000
;      TELEFAX:  312/715-1234
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-418-123A-12

  Query Match             0.4%;  Score 23.4;  DB 1;  Length 37;
  Best Local Similarity   81.8%;  Pred. No. 4.9e+03;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    263 CCCCCCCCTCTCTCTTTCTCTCTCTCTCT 295
          | | ||| |||||||| |||||||| ||||||
Db      2 CGCACCCATCTCTCTCCTTCTCTCTTCCTCTCT 34


RESULT 15
US-08-418-123A-11
; Sequence 11, Application US/08418123A
; Patent No. 5739308
;  GENERAL INFORMATION:
;    APPLICANT:  Kandimalla, Ekambar R.
;    APPLICANT:  Agrawal, Sudhir
;    TITLE OF INVENTION:  Integrated Oligonucleotides
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 7.0 for Windows 95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/418,123A
;      FILING DATE:  April 6, 1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greenfield, Michael S.
;      REGISTRATION NUMBER:  37,142
;      REFERENCE/DOCKET NUMBER:  93,000-E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/715-1000
;      TELEFAX:  312/715-1234
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-418-123A-11

  Query Match             0.4%;  Score 23.4;  DB 1;  Length 38;
  Best Local Similarity   81.8%;  Pred. No. 5e+03;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    263 CCCCCCCCTCTCTCTTTCTCTCTCTCTCT 295
          | | ||| |||||||| |||||||| ||||||
Db      2 CGCACCCATCTCTCTCCTTCTCTCTTCCTCTCT 34


Search completed: March 12, 2003, 02:53:00
Job time : 171 secs
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 21:08:30 ; Search time 315 Seconds
(without alignments)
11180.767 Million cell updates/sec

Title: US-10-003-919-3
Perfect score: 5273
Sequence: 1 ctagggcatggcatcccacg.....aattgtgcctttcttaaaaa 5273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 333959956 residues

Total number of hits satisfying chosen parameters: 261222

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 25.8 | 0.5 | 50 | 10 | US-09-782-650-16 | Sequence 16, Appl |
| | 2 | 25.6 | 0.5 | 37 | 10 | US-09-263-959-766 | Sequence 766, App |
| | 3 | 24.4 | 0.5 | 27 | 10 | US-09-735-363A-6 | Sequence 6, Appli |
| c | 4 | 24.4 | 0.5 | 28 | 10 | US-09-263-959-474 | Sequence 474, App |
| c | 5 | 23.8 | 0.5 | 44 | 10 | US-09-740-002-4 | Sequence 4, Appli |
| c | 6 | 23.4 | 0.4 | 26 | 10 | US-09-263-959-538 | Sequence 538, App |
| c | 7 | 23.4 | 0.4 | 50 | 10 | US-09-740-002-2 | Sequence 2, Appli |
| c | 8 | 23 | 0.4 | 50 | 10 | US-09-740-002-1 | Sequence 1, Appli |
| c | 9 | 22.4 | 0.4 | 24 | 10 | US-09-263-959-862 | Sequence 862, App |
| c | 10 | 21.8 | 0.4 | 44 | 10 | US-09-988-899-55 | Sequence 55, Appl |
| | 11 | 21.6 | 0.4 | 47 | 9 | US-09-853-526-272 | Sequence 272, App |
| | 12 | 21.6 | 0.4 | 47 | 10 | US-09-901-484A-272 | Sequence 272, App |
| | 13 | 21.2 | 0.4 | 42 | 10 | US-09-845-160-13 | Sequence 13, Appl |
| c | 14 | 21.2 | 0.4 | 47 | 10 | US-09-740-002-3 | Sequence 3, Appli |
| | 15 | 21 | 0.4 | 50 | 9 | US-10-087-523-44 | Sequence 44, Appl |
| | 16 | 20.6 | 0.4 | 45 | 9 | US-09-925-922-12 | Sequence 12, Appl |
| c | 17 | 20.6 | 0.4 | 49 | 10 | US-09-740-002-5 | Sequence 5, Appli |
| | 18 | 20.6 | 0.4 | 50 | 9 | US-09-996-956-6 | Sequence 6, Appli |
| c | 19 | 20.6 | 0.4 | 50 | 10 | US-09-740-002-7 | Sequence 7, Appli |
| c | 20 | 20.4 | 0.4 | 49 | 10 | US-09-740-002-10 | Sequence 10, Appl |
| c | 21 | 20.2 | 0.4 | 49 | 10 | US-09-740-002-9 | Sequence 9, Appli |
| | 22 | 20.2 | 0.4 | 49 | 10 | US-09-867-193-8 | Sequence 8, Appli |
| | 23 | 20 | 0.4 | 38 | 9 | US-09-864-785-1279 | Sequence 1279, Ap |
| c | 24 | 20 | 0.4 | 38 | 10 | US-09-884-877-5 | Sequence 5, Appli |
| | 25 | 20 | 0.4 | 47 | 9 | US-09-853-526-195 | Sequence 195, App |
| | 26 | 20 | 0.4 | 47 | 10 | US-09-901-484A-195 | Sequence 195, App |
| c | 27 | 19.8 | 0.4 | 25 | 9 | US-09-863-806-120 | Sequence 120, App |
| | 28 | 19.8 | 0.4 | 37 | 9 | US-09-788-268-13 | Sequence 13, Appl |
| | 29 | 19.8 | 0.4 | 42 | 9 | US-09-998-042-4 | Sequence 4, Appli |
| | 30 | 19.8 | 0.4 | 44 | 10 | US-09-875-519A-13 | Sequence 13, Appl |
| | 31 | 19.8 | 0.4 | 48 | 10 | US-09-818-806A-3 | Sequence 3, Appli |
| | 32 | 19.8 | 0.4 | 49 | 10 | US-09-056-160B-39 | Sequence 39, Appl |
| | 33 | 19.6 | 0.4 | 31 | 9 | US-09-912-263-215 | Sequence 215, App |
| | 34 | 19.6 | 0.4 | 47 | 9 | US-09-905-291A-193 | Sequence 193, App |
| | 35 | 19.6 | 0.4 | 47 | 9 | US-09-902-853-193 | Sequence 193, App |
| | 36 | 19.6 | 0.4 | 47 | 9 | US-09-907-824-193 | Sequence 193, App |
| | 37 | 19.6 | 0.4 | 47 | 9 | US-09-907-841-193 | Sequence 193, App |
| | 38 | 19.6 | 0.4 | 47 | 9 | US-09-904-011-193 | Sequence 193, App |
| | 39 | 19.6 | 0.4 | 47 | 9 | US-09-906-742-193 | Sequence 193, App |
| | 40 | 19.6 | 0.4 | 47 | 9 | US-09-906-838-193 | Sequence 193, App |
| | 41 | 19.6 | 0.4 | 47 | 9 | US-09-907-613-193 | Sequence 193, App |
| | 42 | 19.6 | 0.4 | 47 | 9 | US-09-907-942-193 | Sequence 193, App |
| | 43 | 19.6 | 0.4 | 47 | 9 | US-09-904-820-193 | Sequence 193, App |
| | 44 | 19.6 | 0.4 | 47 | 9 | US-09-904-859-193 | Sequence 193, App |
| | 45 | 19.6 | 0.4 | 47 | 9 | US-09-909-204-193 | Sequence 193, App |

ALIGNMENTS

RESULT 1
US-09-782-650-16/c
; Sequence 16, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dorner, Friedrich
; APPLICANT: Edwards LifeSciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:annealed
; OTHER INFORMATION: oligonucleotide
US-09-782-650-16

Query Match 0.5%; Score 25.8; DB 10; Length 50;
Best Local Similarity 73.3%; Pred. No. 1.6e+03;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 3898 ACCAGCAGACCCCGCCCACCCCGACGCCGCGGCCGCCGCTGCCAG 3942
Db 48 AGCCGCCGCCGCCGCTGCCGCCGCCGCCGCTGCCGCCGCCGCCAG 4

RESULT 2

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US-09-263-959-766
; Sequence 766, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  766:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-766

  Query Match             0.5%;  Score 25.6;  DB 10;  Length 37;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+03;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   4408 ATATAGATAATAATAATATTAATAATAATAAT 4439
          |||  |||||||||||| ||||||||||||||
Db      2 ATAATAATAATAATAATAATAATAATAATAAT 33


RESULT 3
US-09-735-363A-6
; Sequence 6, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
;  APPLICANT: Filion, Mario
;  APPLICANT:  Phillip, Nigel
;  TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
;  FILE REFERENCE: 02811-0181
;  CURRENT APPLICATION NUMBER: US/09/735,363A
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER: 60/170,325
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: 60/228,925
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-6

  Query Match             0.5%;  Score 24.4;  DB 10;  Length 27;
  Best Local Similarity   96.2%;  Pred. No. 2.5e+03;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    270 CTCTCTCTCTTTCTCTCTCTCTCTCT 295
          |||||||||| ||||||||||||||||
Db      2 CTCTCTCTCTCTCTCTCTCTCTCTCT 27


RESULT 4
US-09-263-959-474/c
; Sequence 474, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  474:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-474

  Query Match             0.5%;  Score 24.4;  DB 10;  Length 28;
  Best Local Similarity   96.2%;  Pred. No. 2.6e+03;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   4414 ATAATAATAATATTAATAATAATAAT 4439
          |||||||||||| ||||||||||||
Db     28 ATAATAATAATAATAATAATAATAAT 3


RESULT 5
US-09-740-002-4/c
; Sequence 4, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
```

```
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-740-002-4

  Query Match           0.5%;  Score 23.8;  DB 10;  Length 44;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+03;
  Matches   28;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    255 GGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCT 289
          || |||| | | |  |||||||||| |||||||||
Db     35 GGACAGGACACGCGTCTCTCTCTCTCTCTCTCT 1


RESULT 6
US-09-263-959-538/c
; Sequence 538, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  538:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-538

  Query Match           0.4%;  Score 23.4;  DB 10;  Length 26;
  Best Local Similarity   96.0%;  Pred. No. 4.6e+03;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    271 TCTCTCTCTTTCTCTCTCTCTCTCT 295
          |||||||||| ||||||||||||||||
Db     26 TCTCTCTCTCTCTCTCTCTCTCTCT 2


RESULT 7
US-09-740-002-2/c
; Sequence 2, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-740-002-2

  Query Match           0.4%;  Score 23.4;  DB 10;  Length 50;
  Best Local Similarity   77.1%;  Pred. No. 7.2e+03;
  Matches   27;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    255 GGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCT 289
          || ||:| | | |  |||||||||| |||||||||
Db     35 GGACARGACACGCGTCTCTCTCTCTCTCTCTCT 1


RESULT 8
US-09-740-002-1/c
; Sequence 1, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-740-002-1

  Query Match           0.4%;  Score 23;  DB 10;  Length 50;
  Best Local Similarity   74.3%;  Pred. No. 9.3e+03;
  Matches   26;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    255 GGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCT 289
          || : ||:| | |  |||||||||| |||||||||
Db     35 GGASTGGRCACGCGTCTCTCTCTCTCTCTCTCT 1


RESULT 9
```

```
US-09-263-959-862/c
; Sequence 862, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  862:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-862

  Query Match             0.4%;  Score 22.4;  DB 10;  Length 24;
  Best Local Similarity   95.8%;  Pred. No. 8.3e+03;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    4416 AATAATAATATTAATAATAATAAT 4439
           ||||||||||  ||||||||||||
Db      24 AATAATAATAATAATAATAATAAT 1


RESULT 10
US-09-988-899-55/c
; Sequence 55, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
;  APPLICANT: HOOGENBOOM, HENDRICUS R.J.M.
;  TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
;  FILE REFERENCE: DX/003 CON
;  CURRENT APPLICATION NUMBER: US/09/988,899
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: PCT/US00/13682
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 99201558.6
;  PRIOR FILING DATE: 1999-05-18
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-988-899-55

  Query Match             0.4%;  Score 21.8;  DB 10;  Length 44;
  Best Local Similarity   67.4%;  Pred. No. 1.8e+04;
  Matches   29;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    2524 GTGACCGAGTCCTCTGGAAGTCTTATCCCCTGGTGCACGTGGT 2566
           | ||| | ||| :||||| |||   | | |||||| | | |||
Db      43 GAGACTGGGTCAWCTGGATGTCAAGTGCACTGGTGGAGGCGGT 1


RESULT 11
US-09-853-526-272
; Sequence 272, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Ilya, Chumakov
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/853,526
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 272
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID195
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: base G ; A in SEQ ID195
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 4-38-63.misl
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mis2
US-09-853-526-272

  Query Match             0.4%;  Score 21.6;  DB 9;  Length 47;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+04;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    2144 AAGTGAAAAGAAACTCAGGCGAAACCAAAACTATAT 2179
           |||| | |||||| |||||||  |  | |||||  | |
Db       4 AAGTTATAAGAAAATCAGGCGGAGGCTAAACTTTTT 39


RESULT 12
US-09-901-484A-272
; Sequence 272, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate Cancer Gene
;  FILE REFERENCE: GEN-T111XC3D2
;  CURRENT APPLICATION NUMBER: US/09/901,484A
;  CURRENT FILING DATE:  2001-07-09
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;  PRIOR APPLICATION NUMBER: US 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: US 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: US 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: US 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: US 09/853,526
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 272
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (1)..(47)
;   OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID 195
;   NAME/KEY: allele
;   LOCATION: (24)..(24)
;   OTHER INFORMATION: polymorphic base G; A in SEQ ID 195
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(23)
;   OTHER INFORMATION: potential microsequencing oligo 4-38-63.mis1
;   NAME/KEY: primer_bind
;   LOCATION: (25)..(47)
;   OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mis2
US-09-901-484A-272

  Query Match             0.4%;  Score 21.6;  DB 10;  Length 47;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+04;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    2144 AAGTGAAAAGAAACTCAGGCGAAACCAAAACTATAT 2179
           |||| | |||||| |||||||  |  | ||||| | |
Db       4 AAGTTATAAGAAAATCAGGCGGAGGCTAAACTTTTT 39


RESULT 13
US-09-845-160-13
; Sequence 13, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
;  APPLICANT: MIZUGUCHI, HIROYUKI
;  APPLICANT:  HAYAKAWA, TAKAO
;  TITLE OF INVENTION: ADENOVIRUS VECTOR
;  FILE REFERENCE: 081356/0163
;  CURRENT APPLICATION NUMBER: US/09/845,160
;  CURRENT FILING DATE:  2001-05-01
;  PRIOR APPLICATION NUMBER: JP 2001-131688
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: JP 2000-161577
;  PRIOR FILING DATE: 2000-05-31
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide 7.
US-09-845-160-13

  Query Match             0.4%;  Score 21.2;  DB 10;  Length 42;
  Best Local Similarity   69.0%;  Pred. No. 2.6e+04;
  Matches   29;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    3922 CGCCGCGGCCGCCGCTGCCAGTCAAGAGCCCGGCGGTGCTGC 3963
           ||| ||||||| ||| |||  ||| |   | | || ||| ||
Db       1 CGCAGCGGCCGGCGCAGCCGCTCACGCAGCGGCCGTTGCAGC 42


RESULT 14
US-09-740-002-3/c
; Sequence 3, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-740-002-3

  Query Match             0.4%;  Score 21.2;  DB 10;  Length 47;
  Best Local Similarity   76.5%;  Pred. No. 2.8e+04;
  Matches   26;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy     258 CAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCTCT 291
           ||  |  | | | |||||||||| ||||||||||
Db      34 CACTGGACACGCGTCTCTCTCTCTCTCTCTCTCT 1


RESULT 15
US-10-087-523-44
; Sequence 44, Application US/10087523
; Publication No. US20020197624A1
; GENERAL INFORMATION:
;  APPLICANT: Klein, Robert D.
;  APPLICANT:  Brennan, Thomas J.
;  TITLE OF INVENTION: METHODS OF CREATING CONSTRUCTS USEFUL FOR INTRODUCING
;  TITLE OF INVENTION:  SEQUENCES INTO EMBRYONIC STEM CELLS
;  FILE REFERENCE: 376472000200
;  CURRENT APPLICATION NUMBER: US/10/087,523
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/193,834
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-17
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Plasmid vector
US-10-087-523-44

  Query Match             0.4%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 3.4e+04;
  Matches   30;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    4323 CTCGCTCTTGGTACTTGGGACCCCAGTGCCTCGTTGAGGGCGCCA 4367
           |||||||  || | | | || ||||||||  ||    || | ||
Db       5 CTCGCTCTGTGTCCGTTGAACTCCAGTGCCGAGTGTGTGGGGACA 49


Search completed: March 12, 2003, 02:58:30
Job time : 321 secs
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GenCore version 5.1.4_p5_4578


OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 20:47:25 ; Search time 6709 Seconds
(without alignments)
12728.991 Million cell updates/sec

Title: US-10-003-919-3
Perfect score: 5273
Sequence: 1 ctagggcatggcatcccacg.....aattgtgcctttcttaaaaa 5273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 30 | 0.6 | 49 | 10 | AV674036 | AV674036 AV674036 |
| 2 | 30 | 0.6 | 49 | 10 | AV965544 | AV965544 AV965544 |
| 3 | 29.8 | 0.6 | 41 | 17 | AZ424284 | AZ424284 1M0203M14 |
| 4 | 29.6 | 0.6 | 40 | 17 | AZ328467 | AZ328467 1M0052E18 |
| 5 | 29.4 | 0.6 | 47 | 10 | AV949200 | AV949200 AV949200 |
| 6 | 29.2 | 0.6 | 44 | 13 | BJ001599 | BJ001599 BJ001599 |
| 7 | 29.2 | 0.6 | 49 | 17 | AZ846608 | AZ846608 2M0146F20 |
| 8 | 28.6 | 0.5 | 38 | 17 | AZ479185 | AZ479185 1M0299J11 |
| 9 | 28.6 | 0.5 | 47 | 10 | AV947640 | AV947640 AV947640 |
| 10 | 28.4 | 0.5 | 38 | 17 | AZ333216 | AZ333216 1M0062N12 |
| 11 | 28.4 | 0.5 | 47 | 17 | AZ385990 | AZ385990 1M0144D16 |
| 12 | 28.4 | 0.5 | 47 | 17 | AZ853064 | AZ853064 2M0156K04 |
| 13 | 28.4 | 0.5 | 47 | 17 | AZ862836 | AZ862836 2M0170N09 |
| 14 | 28.4 | 0.5 | 47 | 17 | AZ864870 | AZ864870 2M0174M10 |
| 15 | 28.4 | 0.5 | 49 | 9 | AA773360 | AA773360 ab65h08.s |
| 16 | 28.4 | 0.5 | 49 | 9 | AA842027 | AA842027 MBAFCF2D0 |
| c 17 | 28.4 | 0.5 | 49 | 9 | AI813244 | AI813244 3G2 Pine |
| 18 | 28.4 | 0.5 | 49 | 10 | AV833587 | AV833587 AV833587 |
| 19 | 28.4 | 0.5 | 49 | 13 | BJ000259 | BJ000259 BJ000259 |
| 20 | 28.4 | 0.5 | 50 | 17 | AZ374770 | AZ374770 1M0127I18 |
| 21 | 28.2 | 0.5 | 42 | 10 | AV957667 | AV957667 AV957667 |
| 22 | 28.2 | 0.5 | 50 | 17 | AZ665271 | AZ665271 1M0546C08 |
| c 23 | 28 | 0.5 | 44 | 10 | AV833550 | AV833550 AV833550 |
| 24 | 28 | 0.5 | 47 | 17 | AZ649857 | AZ649857 1M0519O08 |
| 25 | 27.8 | 0.5 | 50 | 17 | AZ776590 | AZ776590 2M0010A23 |
| c 26 | 27.6 | 0.5 | 40 | 10 | AV833442 | AV833442 AV833442 |
| c 27 | 27.6 | 0.5 | 42 | 14 | T54684 | T54684 yb41a05.r1 |
| c 28 | 27.6 | 0.5 | 43 | 17 | AZ345546 | AZ345546 1M0080C14 |
| 29 | 27.6 | 0.5 | 44 | 10 | AV672475 | AV672475 AV672475 |
| 30 | 27.6 | 0.5 | 44 | 17 | AZ974579 | AZ974579 2M0249A18 |
| 31 | 27.6 | 0.5 | 47 | 17 | AZ456727 | AZ456727 1M0259D17 |
| c 32 | 27.6 | 0.5 | 50 | 14 | BQ577141 | BQ577141 PfESToab1 |
| c 33 | 27.4 | 0.5 | 49 | 17 | AZ790087 | AZ790087 2M0038H24 |
| c 34 | 27.2 | 0.5 | 32 | 17 | AZ329877 | AZ329877 1M0054L07 |
| c 35 | 27.2 | 0.5 | 32 | 17 | AZ515185 | AZ515185 1M0054L07 |
| c 36 | 27.2 | 0.5 | 40 | 9 | AI073810 | AI073810 oy69d05.x |
| 37 | 27.2 | 0.5 | 41 | 10 | AV672637 | AV672637 AV672637 |
| c 38 | 27.2 | 0.5 | 42 | 17 | AZ826548 | AZ826548 2M0102I02 |
| 39 | 27.2 | 0.5 | 42 | 17 | AZ941720 | AZ941720 2M0201O03 |
| 40 | 27.2 | 0.5 | 47 | 10 | AV955412 | AV955412 AV955412 |
| 41 | 27.2 | 0.5 | 50 | 12 | BE976895 | BE976895 bs57d03.y |
| 42 | 26.8 | 0.5 | 39 | 10 | AV673727 | AV673727 AV673727 |
| c 43 | 26.8 | 0.5 | 49 | 10 | AV671476 | AV671476 AV671476 |
| 44 | 26.4 | 0.5 | 37 | 10 | AV673465 | AV673465 AV673465 |
| 45 | 26.4 | 0.5 | 37 | 17 | AZ346663 | AZ346663 1M0082C01 |

ALIGNMENTS

RESULT 1
AV674036
LOCUS AV674036 49 bp mRNA linear EST 05-OCT-2000
DEFINITION AV674036 Nori Satoh unpublished cDNA library Ciona intestinalis cDNA clone citb14a20 5', mRNA sequence.
ACCESSION AV674036
VERSION AV674036.1 GI:10112035
KEYWORDS EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 49)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1..49
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="citb14a20"
/clone_lib="Nori Satoh unpublished cDNA library"

/tissue_type="whole animal"
/dev_stage="tailbud"
/note="Vector: pBluescript SK"
BASE COUNT 2 a 22 c 5 g 20 t
ORIGIN

Query Match 0.6%; Score 30; DB 10; Length 49;
Best Local Similarity 78.3%; Pred. No. 1.3e+04;
Matches 36; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 254 CGGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCT 299
|||| | | | | | |||||||||| ||||||||||||||| ||
Db 3 CGGCACGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 48

RESULT 2
AV965544
LOCUS AV965544 49 bp mRNA linear EST 14-MAR-2002
DEFINITION AV965544 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg19i14 5', mRNA sequence.
ACCESSION AV965544
VERSION AV965544.1 GI:19455240
KEYWORDS EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 49)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .49
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="cieg19i14"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/note="Vector: pBluescript SK"
BASE COUNT 2 a 22 c 5 g 20 t
ORIGIN

Query Match 0.6%; Score 30; DB 10; Length 49;
Best Local Similarity 78.3%; Pred. No. 1.3e+04;
Matches 36; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 254 CGGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCT 299
|||| | | | | | |||||||||| ||||||||||||||| ||
Db 2 CGGCACGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47

RESULT 3
AZ424284
LOCUS AZ424284 41 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0203M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0203M14 R, DNA sequence.
ACCESSION AZ424284
VERSION AZ424284.1 GI:10548297
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: M column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
FEATURES Location/Qualifiers
source 1. .41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203M14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 19 c 0 g 22 t
ORIGIN

Query Match 0.6%; Score 29.8; DB 17; Length 41;
Best Local Similarity 82.9%; Pred. No. 1.3e+04;
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 266 CCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTC 306
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Db 1 CCCTCCCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTC 41

RESULT 4
AZ328467
LOCUS AZ328467 40 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0052E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0052E18 F, DNA sequence.
ACCESSION AZ328467
VERSION AZ328467.1 GI:10388225
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

```
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0052  row: E  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES              Location/Qualifiers
     source           1. .40
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0052E18"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       1 a      19 c       0 g      20 t
ORIGIN

  Query Match             0.6%;  Score 29.6;  DB 17;  Length 40;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+04;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTGCT 299
           | | |||||||||||||| |||||||||||||||| ||
Db       5 CTCTCCCTCTCTCTCTCTCTCTCTCTCTCTTTCT 40


RESULT 5
AV949200
LOCUS       AV949200                  47 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV949200 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone cilv02g12 5', mRNA sequence.
ACCESSION   AV949200
VERSION     AV949200.1  GI:19437499
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Ciona intestinalis"
                      /db_xref="taxon:7719"
                      /clone="cilv02g12"
                      /clone_lib="Nori Satoh unpublished cDNA library, larva"
                      /tissue_type="whole animal"
                      /dev_stage="larva"
                      /note="Vector: pBluescript SK"
BASE COUNT       1 a      23 c       0 g      23 t
ORIGIN

  Query Match             0.6%;  Score 29.4;  DB 10;  Length 47;
  Best Local Similarity   76.6%;  Pred. No. 1.8e+04;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTTGCTTGGTTTCTGTA 310
           | | | |||||||||| |||||||||||||||  ||   | ||| ||
Db       1 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTA 47


RESULT 6
BJ001599
LOCUS       BJ001599                  44 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ001599 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA009H08 5',
            mRNA sequence.
ACCESSION   BJ001599
VERSION     BJ001599.1  GI:17364490
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .44
                      /organism="Oryzias latipes"
                      /strain="Hd-rR"
                      /db_xref="taxon:8090"
                      /clone="MF01SSA009H08"
                      /clone_lib="MF01SSA cDNA"
                      /sex="mixture of female and male"
                      /tissue_type="whole embryo"
                      /dev_stage="segmentation stage 20 - 25"
BASE COUNT       2 a      20 c       5 g      17 t
ORIGIN

  Query Match             0.6%;  Score 29.2;  DB 13;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 1.9e+04;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy     254 CGGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCTCTCT 295
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Db      2 CGGCACGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 43


RESULT 7
AZ846608
LOCUS       AZ846608                 49 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0146P20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0146P20 R, DNA sequence.
ACCESSION   AZ846608
VERSION     AZ846608.1  GI:13027870
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0146  row: F  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0146P20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        2 a     20 c      3 g     24 t
ORIGIN

  Query Match             0.6%;  Score 29.2;  DB 17;  Length 49;
  Best Local Similarity   81.0%;  Pred. No. 2e+04;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    268 CCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
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Db      7 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGT 48


RESULT 8
AZ479185
LOCUS       AZ479185                 38 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0299J11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0299J11 R, DNA sequence.
ACCESSION   AZ479185
VERSION     AZ479185.1  GI:10638641
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0299  row: J  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0299J11"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a     18 c      1 g     19 t
ORIGIN

  Query Match             0.5%;  Score 28.6;  DB 17;  Length 38;
  Best Local Similarity   88.6%;  Pred. No. 2.6e+04;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    264 CCCCCCCTCTCTCTTTCTCTCTCTCTCTTGC 298
```

```
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Db      4 CTCTCTCTCTCTCTCTCTCTCTCTCTCTTGC 38


RESULT 9
AV947640
LOCUS       AV947640                 47 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV947640 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad01g16 5', mRNA sequence.
ACCESSION   AV947640
VERSION     AV947640.1  GI:19425399
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="ciad01g16"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /note="Vector: pBluescript SK"
BASE COUNT        0 a      23 c       0 g      23 t       1 others
ORIGIN

  Query Match             0.5%;  Score 28.6;  DB 10;  Length 47;
  Best Local Similarity   77.3%;  Pred. No. 2.8e+04;
  Matches   34;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTTGCTTGGTTTCT 307
           | | | |||||||||| |||||||||||||||  ||    | |||
Db       3 CTCTCTCTCTCTCTCTNTCTCTCTCTCTCTCTCTCTCTCTCT 46


RESULT 10
AZ333216
LOCUS       AZ333216                 38 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0062N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0062N12 F, DNA sequence.
ACCESSION   AZ333216
VERSION     AZ333216.1  GI:10397615
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0062  row: N  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0062N12"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      19 c       1 g      18 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 17;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+04;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     262 GCCCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTCTTGCT 299
           ||| | | |||||||||| ||||||||||||||||  ||
Db       1 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 38


RESULT 11
AZ385990
LOCUS       AZ385990                 47 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0144D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0144D16 R, DNA sequence.
ACCESSION   AZ385990
VERSION     AZ385990.1  GI:10499690
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0144  row: D  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0144D16"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        0 a      23 c       0 g      24 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 17;  Length 47;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+04;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
          | | | |||||||||| |||||||||||||||  ||   | ||| |
Db      2 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47


RESULT 12
AZ853064
LOCUS       AZ853064                47 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0156K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0156K04 F, DNA sequence.
ACCESSION   AZ853064
VERSION     AZ853064.1  GI:13040804
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0156  row: K  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0156K04"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        0 a      23 c       0 g      24 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 17;  Length 47;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+04;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
          | | | |||||||||| |||||||||||||||  ||   | ||| |
Db      2 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47


RESULT 13
AZ862836
LOCUS       AZ862836                47 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0170N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0170N09 R, DNA sequence.
ACCESSION   AZ862836
VERSION     AZ862836.1  GI:13060537
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0170  row: N  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0170N09"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        0 a      23 c       0 g      24 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 17;  Length 47;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+04;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
           | | | ||||||||||  |||||||||||||||  ||   | ||| |
Db       2 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47


RESULT 14
AZ864870
LOCUS       AZ864870                47 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0174M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0174M10 R, DNA sequence.
ACCESSION   AZ864870
VERSION     AZ864870.1  GI:13064604
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0174  row: M  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0174M10"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        0 a      23 c       0 g      24 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 17;  Length 47;
  Best Local Similarity   76.1%;  Pred. No. 3.1e+04;
  Matches   35;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
           | | | ||||||||||  |||||||||||||||  ||   | ||| |
Db       2 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47


RESULT 15
AA773360
LOCUS       AA773360                49 bp    mRNA    linear   EST 29-JAN-1998
DEFINITION  ab65h08.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone
            IMAGE:845727 3' similar to gb:X63657_rna1 FOLLICULAR VARIANT
            TRANSLOCATION PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AA773360
VERSION     AA773360.1  GI:2824931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
```

```
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Trace considered overall poor quality
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:845727"
                     /clone_lib="Stratagene lung carcinoma 937218"
                     /tissue_type="lung carcinoma"
                     /cell_line="NCI-H69"
                     /dev_stage="cell line NCI-H69"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
                     ; Site_2: XhoI; Cloned unidirectionally.  Primer: Oligo
                     dT. Small cell carcinoma cell line NCI-H69.  Average
                     insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT        0 a     15 c      3 g     31 t
ORIGIN

  Query Match             0.5%;  Score 28.4;  DB 9;  Length 49;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+04;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     270 CTCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCT 307
           |||||||||| ||||||||||||||  |||  ||| |
Db       2 CTCTCTCTCTCTCTCTCTCTCTCTCTCTTTTTTTTT 39


Search completed: March 12, 2003, 02:50:06
Job time : 6721 secs
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